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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/779,334A

DATE: 07/26/2001

TIME: 17:42:48

Input Set : A:\NOVT 100.ST25.txt

Output Set: N:\CRF3\07262001\I779334A.raw

ENTERED

3 <110> APPLICANT: Sjoeholm, Carsten
 4 Oestergaard, Peter Rahbek
 5 Kluenter, Anne-Marie
 7 <120> TITLE OF INVENTION: Use of Acid-Stable Subtilisin Proteases in Animal Feed
 9 <130> FILE REFERENCE: NOVT 100
 11 <140> CURRENT APPLICATION NUMBER: 09/779,334A
 12 <141> CURRENT FILING DATE: 2001-02-08
 14 <160> NUMBER OF SEQ ID NOS: 7
 16 <170> SOFTWARE: PatentIn version 3.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 27
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Acremonium chrysogenum ATCC 48272
 23 <400> SEQUENCE: 1
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 26 1 5 10 15
 29 His Arg Gln Pro Gly Ser Thr Ser Tyr Ile Tyr
 30 20 25
 33 <210> SEQ ID NO: 2
 34 <211> LENGTH: 17
 35 <212> TYPE: PRT
 36 <213> ORGANISM: Bacillus alcalophilus NCIMB 10438
 38 <400> SEQUENCE: 2
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 44 Trp
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 49 <211> LENGTH: 17
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Paecilomyces lilacinus CBS 102449
 53 <400> SEQUENCE: 3
 55 Ala Tyr Thr Gln Gln Pro Gly Ala Pro Trp Gly Leu Gly Arg Ile Ser
 56 1 5 10 15
 59 His
 63 <210> SEQ ID NO: 4
 64 <211> LENGTH: 22
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Fusarium oxysporum IFO 4471
 68 <400> SEQUENCE: 4
 70 Ala Leu Thr Thr Gln Ser Gly Ala Thr Trp Gly Leu Gly Thr Val Ser

71 <210> SEQ ID NO: 5
 72 <211> LENGTH: 18
 73 <212> TYPE: PRT
 74 <213> ORGANISM: Bacillus sp. NCIMB 4143

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83 <220> FEATURE:

84 <221> NAME/KEY: SIGNAL

85 <222> LOCATION: (1)..(27)

86 <223> OTHER INFORMATION:

89 <220> FEATURE

90 <221> NAME/KEY: PEPTIDE

91 <222> LOCATION: (118)..(397)

92 <223> OTHER INFORMATION:

95 <220> FEATURE:

96 <221> NAME/KEY: mat_peptide

97 <222> LOCATION: (28)..()

98 <223> OTHER INFORMATION:

101 <400> SEQUENCE: 5

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107 Leu Phe Pro Ala Phe Gly Gly Ser Ser Leu Ala Lys Glu Ala Pro Lys
108      -10      -5      -1 1      5
111 Pro Phe Gln Pro Ile Asn Lys Thr Leu Asp Lys Gly Ala Phe Glu Ser
112      10      15      20
115 Gly Glu Val Ile Val Lys Phe Lys Asp Gly Val Ser Lys Lys Ala Gln
116      25      30      35
119 Gly Ser Ala Leu Asn Lys Ala Glu Ala Asn Glu Gln Lys Ala Ser Ala
120      40      45      50
123 Lys Asp Pro Phe Gln Val Leu Glu Val Ala Asp Val Asp Gln Ala Val
124      55      60      65
127 Lys Ala Leu Glu Asn Asn Pro Asn Val Glu Tyr Ala Glu Pro Asn Tyr
128 70      75      80      85
131 Thr Phe Gln Ala Thr Trp Ser Pro Asn Asp Pro Tyr Tyr Ser Ala Tyr
132      90      95      100
135 Gln Tyr Gly Pro Gln Asn Thr Ser Thr Pro Ala Ala Trp Asp Val Thr
136      105      110      115
139 Arg Gly Ser Ser Thr Gln Thr Val Ala Val Leu Asp Ser Gly Val Asp
140      120      125      130
143 Tyr Asn His Pro Asp Leu Ala Arg Lys Val Ile Lys Gly Tyr Asp Phe
144      135      140      145
147 Ile Asp Arg Asp Asn Asn Pro Met Asp Leu Asn Gly His Gly Thr His
148 150      155      160      165
151 Val Ala Gly Thr Val Ala Ala Asp Thr Asn Asn Gly Ile Gly Val Ala
152      170      175      180
155 Gly Met Ala Pro Asp Thr Lys Ile Leu Ala Val Arg Val Leu Asp Ala
156      185      190      195
159 Asn Gly Ser Gly Ser Leu Asp Ser Ile Ala Ser Gly Ile Arg Tyr Ala
160      200      205      210
163 Ala Asp Gln Gly Ala Lys Val Leu Asn Leu Ser Leu Gly Cys Glu Cys
164      215      220      225

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175 Gln Pro Ala Ser Tyr Pro Asn Ala Ile Ala Val Gly Ala Ile Asp Ser
176          265          270          275
179 Asn Asp Arg Lys Ala Ser Phe Ser Asn Tyr Gly Thr Trp Val Asp Val
180          280          285          290
183 Thr Ala Pro Gly Val Asn Ile Ala Ser Thr Val Pro Asn Asn Gly Tyr
184          295          300          305
187 Ser Tyr Met Ser Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Leu
188 310          315          320          325
191 Ala Ala Leu Leu Ala Ser Gln Gly Lys Asn Asn Val Gln Ile Arg Gln
192          330          335          340
195 Ala Ile Glu Gln Thr Ala Asp Lys Ile Ser Gly Thr Gly Thr Asn Phe
196          345          350          355
199 Lys Tyr Gly Lys Ile Asn Ser Asn Lys Ala Val Arg Tyr
200          360          365          370

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203 <210> SEQ ID NO: 6

204 <211> LENGTH: 367

205 <212> TYPE: PRT

206 <213> ORGANISM: Paecilomyces lilacinus CBS 143.75

208 <220> FEATURE:

209 <221> NAME/KEY: PEPTIDE

210 <222> LOCATION: (70)..(367)

211 <223> OTHER INFORMATION:

214 <220> FEATURE:

215 <221> NAME/KEY: PEPTIDE

216 <222> LOCATION: (84)..(367)

217 <223> OTHER INFORMATION:

220 <400> SEQUENCE: 6

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222 Ala Arg Ala Pro Leu Leu Thr Pro Arg Gly Ala Ser Ser Ser Ser Thr
223 1          5          10          15
226 Ala Ser Thr Leu Ser Ser Ser Arg Thr Ala Cys Pro Ser Pro Leu Ser
227          20          25          30
230 Thr Arg Leu Ser Ala Leu Cys Pro Arg Arg Pro Thr Ala Ser Thr Thr
231          35          40          45
234 Thr Phe Ser Glu Ala Ser Arg Asn Leu Asn Ala Asn Asp Leu Lys Thr
235          50          55          60
238 Leu Arg Asp His Pro Asp Val Glu Tyr Ile Glu Gln Asp Ala Ile Ile
239 65          70          75          80
242 Thr Ile Asn Ala Tyr Thr Gln Gln Pro Gly Ala Pro Trp Gly Leu Gly
243          85          90          95
246 Arg Ile Ser His Arg Ser Lys Gly Ser Thr Thr Tyr Glu Tyr Asp Thr
247          100          105          110
250 Ser Gly Gly Ser Gly Thr Cys Ala Tyr Val Ile Asp Thr Gly Val Glu
251          115          120          125
254 Ala Ser His Pro Glu Phe Glu Gly Arg Ala Ser Gln Ile Lys Ser Phe
255          130          135          140

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266 Tyr Gly Val Lys Val Leu Asp Asn Ser Gly Ser Gly Ser Tyr Ser Gly
267          180          185          190
270 Ile Ile Ser Gly Met Asp Phe Ala Val Gln Asp Ser Lys Ser Arg Ser
271          195          200          205
274 Cys Pro Lys Gly Val Val Ala Asn Met Ser Leu Gly Gly Gly Lys Ala
275          210          215          220
278 Gln Ser Val Asn Asp Gly Ala Ala Ala Met Ile Arg Ala Gly Val Phe
279 225          230          235          240
282 Leu Ala Val Ala Ala Gly Asn Asp Asn Ala Asn Ala Ala Asn Tyr Ser
283          245          250          255
286 Pro Ala Ser Gln Pro Thr Val Cys Thr Val Gly Ala Thr Thr Ser Ser
287          260          265          270
290 Asp Ala Arg Ser Ser Phe Ser Asn Tyr Gly Asn Leu Val Asp Ile Phe
291          275          280          285
294 Ala Pro Gly Ser Asn Ile Leu Ser Thr Trp Ile Gly Gly Thr Thr Asn
295          290          295          300
298 Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His Ile Val Gly Leu Gly
299 305          310          315          320
302 Ala Tyr Leu Ala Gly Leu Glu Gly Phe Pro Gly Ala Gln Ala Leu Cys
303          325          330          335
306 Lys Arg Ile Gln Thr Leu Ser Thr Lys Asn Val Leu Thr Gly Ile Pro
307          340          345          350
310 Ser Gly Thr Val Asn Tyr Leu Ala Phe Asn Gly Asn Pro Ser Gly
311          355          360          365
314 <210> SEQ ID NO: 7
315 <211> LENGTH: 269
316 <212> TYPE: PRT
317 <213> ORGANISM: Bacillus sp. THS-1001
319 <400> SEQUENCE: 7
321 Asn Gln Val Thr Pro Trp Gly Ile Thr Arg Val Gln Ala Pro Thr Ala
322 1          5          10          15
325 Trp Thr Arg Gly Tyr Thr Gly Thr Gly Val Arg Val Ala Val Leu Asp
326          20          25          30
329 Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Val Ser
330          35          40          45
333 Phe Val Pro Gly Glu Pro Ser Tyr Gln Asp Gly Asn Gly His Gly Thr
334          50          55          60
337 His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Val
338 65          70          75          80
341 Gly Val Ala Pro Asn Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
342          85          90          95
345 Asn Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Gln Trp Thr
346          100          105          110
349 Ala Gln Asn Asn Ile His Val Ala Asn Leu Ser Leu Gly Ser Pro Val
          115          120          125

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361 Tyr Pro Ala Arg Tyr Ala Asn Ala Leu Ala Val Gly Ala Thr Asp Gln
362                165                170                175
365 Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Thr Gly Leu Asn Ile
366                180                185                190
369 Val Ala Pro Gly Val Gly Ile Gln Ser Thr Tyr Pro Gly Asn Arg Tyr
370                195                200                205
373 Ala Ser Leu Ser Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Val
374        210                215                220
377 Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Thr Gln Ile
378 225                230                235                240
381 Arg Gln His Leu Thr Ser Thr Ala Thr Ser Leu Gly Asn Ser Asn Gln
382                245                250                255
385 Phe Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
386                260                265

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VERIFICATION SUMMARY

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